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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:18:03 ; Search time 1404.05 Seconds
(without alignments)
12007.805 Million cell updates/sec

Title: US-09-807-933B-12
Perfect score: 1041
Sequence: 1 atgaagttctccatcatgcg.....ctggttgcgagcgaagtaa 1041

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163.2	15.7	691	10	BES85661
2	115.8	11.1	450	13	BI200729
3	111	10.7	972	17	CNS02QMI
4	107	10.3	540	17	AZ583039
5	106.4	10.2	723	17	AZ627893
6	106.2	10.2	444	13	BI190695

7	103.8	10.0	498	17	AQ927406
8	103.4	9.9	597	17	AQ2764733
9	102.4	9.8	400	17	AZ000660
10	102.2	9.8	769	17	AG077414
11	102	9.8	279	17	CNS03W9F
12	101	9.7	810	17	CNS0272N
13	100.6	9.7	536	17	CNS03QOK
14	98.8	9.5	426	13	BI187295
15	98.2	9.4	529	17	AQ759124
16	97.8	9.4	708	17	AZ938145
17	97.4	9.4	408	9	AA484400
18	97	9.3	522	13	BI783235
19	96.6	9.3	630	17	CNS04HMV
20	96	9.2	447	17	BH094533
21	95.8	9.2	325	17	CNS03PK8
22	95.6	9.2	590	17	CNS03M2Z
23	94	9.0	745	17	BH500565
24	93.4	9.0	303	9	AA613152
25	92.4	8.9	998	17	BH133989
26	90.2	8.7	772	17	CNS02CCA
27	89.8	8.6	868	17	BH162606
28	89	8.5	512	13	EM034492
29	88.8	8.5	695	17	AZ262582
30	88.6	8.5	790	17	CNS0379X
31	88.4	8.5	511	17	AQ487936
32	87.8	8.4	284	17	CNS024VK
33	87.4	8.4	572	17	CNS043SN
34	87.4	8.4	723	17	AZ966297
35	87.2	8.4	774	17	CNS02APC
36	87.2	8.4	876	17	BH161693
37	86.8	8.3	884	17	CNS02NX2
38	86.6	8.3	703	17	AZ986572
39	86.4	8.3	330	14	D16000
40	86.4	8.3	426	14	D22721
41	86	8.3	821	17	CNS03F7F
42	85.8	8.2	329	9	AI668748
43	85.4	8.2	442	14	BQ622552
44	85.2	8.2	265	14	BQ985384
45	85	8.2	712	17	CNS04AL2

ALIGNMENTS

RESULT 1
BES85661
LOCUS
DEFINITION
BES85661 691 bp mRNA linear EST 17-AUG-2000
EST#6PSP6_D02_d2_014 KSU wheat Fusarium graminearum infected spike
CDNA library Triticum aestivum CDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BES85661 GI:9838604
EST.
Triticum aestivum
bread wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE
AUTHORS
TITLE
Fellers, J.P., Li, W.L., Hill-Ambroz, K., Matthews, A. and Gill, B.S.
The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike cDNA library
JOURNAL
COMMENT
Unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed to remove vector sequence and low

D	b		331	ACACCACTATCACACCACCCAGCACCACCATTCATTACCAACCACCAACGACCAACC	390
Q	y		319	ACTTACTACTACCAACCACAAAGACACACACAAGAACAACACCAACCAAGGTGCACACAC	378
D	b		391	ACTATCACCAACCACCAACCGACCAACCATTTATCACCACCAACCAACGACCAACCAAGCACC	450
Q	y		379	ACCTCTCTTCACACACTGGCTACAGGCCCATTTCTGGTGCTCTCTGGAACCGGTGC	438
D	b		451	ACTAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	510
Q	y		439	ACTACCGGCTAC	450
D	b		511	ACCACCAACAAC	522
RESULT 6					
BI190695					
LOCUS					
DEFINITION					
BI190695 444 bp mRNA EST 10-JUL-2000 ig3l0fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone ig3l0fs 5', mRNA sequence.					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
FEATURES					
source					
1..444					
/organism="Fusarium sporotrichioides"					
/strain="Tri 10"					
/db_xref="taxon:5514"					
/cclone="ig3l0fs"					
/cloned_lib="Fusarium sporotrichioides Tri 10 overexpresses cDNA library"					
/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pluescript" 3' , end of cDNA cloned into XhoI site of pluescript"					
BASE COUNT					
ORIGIN					
Query Match Score 106.2; DB 13; Length 444;					
Best Local Similarity 63.1%; Pred.No. 2.1e-13;					
Matches 181; Conservative 0; Mismatches 103; Indels 3; Gaps 1;					
Q	y	424	TCTGGAAA	CAGTTCGACTACCCCTACTGGATTGCTGCAAGCCCTCTTGCGCTGGGAC	488
D	b	158	TCTGGAAGTGGCCACTCTACTCGATACTGGGACTGCTGCAAGCCTTCTTGCTTGGAGC	211	
Q	y	484	GGAAGGCTTCTGTACTAAGCCTGTACTCACCTGTGCCAAGGATGTTGTC---AGCGGT	541	
D	b	218	GGCAAGGCTAAAGTCAGCGCCCCTGCTGACTTGTGACAAACAAGATAACCCCTATCACT	271	
Q	y	541	CTCGTTCCGATGTCAGACGGTTGGCTCGCGGCCAGCGCCTACATGTGCAATGACAAC	601	

AZ627893 723 bp DNA linear GSS 13-DEC-2000
IM0469118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0469118 R, DNA sequence.
AZ627893
AZ627893.1 GI:11749999
GSS
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 723)
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
. M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0469 row: I column: 18
Seq primer: CACACAGGAACACTATGACC
Class: plasmid ends
High quality sequence stop: 723.

FEATURES

source

1..723
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0469118"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/note=vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
[\(http://www.jax.org/resources/documents/dnares/\)](http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid r1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 257 a 266 c 74 g 126 t

ORIGIN

Query Match 10.2%; Score 106.4; DB 17; Length 723;
Best Local Similarity 63.9%; Pred. No. 2.5e-13;
Matches 161; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 199 AACCCCAAGACACCAACCACCAACCACCAAGGTGGCATTACCACAAGGCTCTGTC 258
DB 271 ACCACGACCAACCACTATTACCACCAACCAACCACTATCACCAACCACCGAC 330

QY 259 ACCACCAAGGCCACCAACCACCAACCACCAAGGCCCTTGTCACCAACCACCAAGCCC 318

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